

Sequence listing

Sequence No. : 1

Sequence length: 180

5 Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Sequence description

10 GGA AAG CTC CCT TTC TCA AGA ATG CCC ATC TGT GAA CAC ATG GTA GAG 48  
 Gly Lys Leu Pro Phe Ser Arg Met Pro Ile Cys Glu His Met Val Glu  
 1 5 10 15  
 TCT CCA ACC TGT TCC CAG ATG TCC AAC CTG GTC TGC GGC ACT GAT GGG 96  
 15 Ser Pro Thr Cys Ser Gln Met Ser Asn Leu Val Cys Gly Thr Asp Gly  
 20 25 30  
 CTC ACA TAT ACG AAT GAA TGC CAG CTC TGC TTG GCC CGG ATA AAA ACC 144  
 Leu Thr Tyr Thr Asn Glu Cys Gln Leu Cys Leu Ala Arg Ile Lys Thr  
 35 40 45  
 20 AAA CAG GAC ATC CAG ATC ATG AAA GAT GGC AAA TGC 180  
 Lys Gln Asp Ile Gln Ile Met Lys Asp Gly Lys Cys  
 50 55 60

25 Sequence No. : 2

Sequence length: 398

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

30 Sequence kind: cDNA to mRNA

Origin:

Animal name: Homo sapiens

Cell kind: Stomach cancer tissue

Clone name: HP00839

35 Sequence characteristics:

Characterization code: CDS

Existence position: 43..303

Sequence description

40 GCAGGCCCCA GCCAGCTCAG GCTACACTAT CCCAGGATCA GC ATG GCC GTC CGC 54

09941309.082801

1

	CAG TGG GTA ATC GCC CTG GCC TTG GCT GCC CTC CTT GTT GTG GAC AGG	102
	Gln Trp Val Ile Ala Leu Ala Leu Ala Ala Leu Leu Val Val Asp Arg	
5	5                      10                      15                      20	
	GAA GTG CCA GTG GCA GCA GGA AAG CTC CCT TTC TCA AGA ATG CCC ATC	150
	Glu Val Pro Val Ala Ala Gly Lys Leu Pro Phe Ser Arg Met Pro Ile	
	25                      30                      35	
	TGT GAA CAC ATG GTA GAG TCT CCA ACC TGT TCC CAG ATG TCC AAC CTG	198
10	Cys Glu His Met Val Glu Ser Pro Thr Cys Ser Gln Met Ser Asn Leu	
	40                      45                      50	
	GTC TGC GGC ACT GAT GGG CTC ACA TAT ACG AAT GAA TGC CAG CTC TGC	246
	Val Cys Gly Thr Asp Gly Leu Thr Tyr Thr Asn Glu Cys Gln Leu Cys	
	55                      60                      65	
15	TTG GCC CGG ATA AAA ACC AAA CAG GAC ATC CAG ATC ATG AAA GAT GGC	294
	Leu Ala Arg Ile Lys Thr Lys Gln Asp Ile Gln Ile Met Lys Asp Gly	
	70                      75                      80	
	AAA TGC TGATCCCACA GGAGCACCTC AAGCCATGAA GTGTCAGCTG GAGAACAGTG	350
	Lys Cys	
20	85	
	GTGGGCATGG AGAGGATATG ACATGAAATA AAAGATCCAG CCCAACTG	398